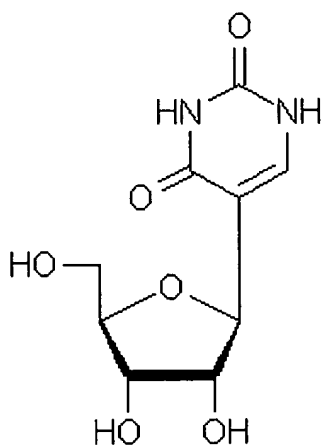
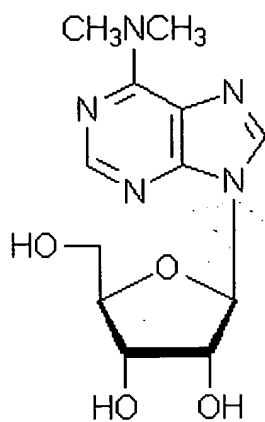
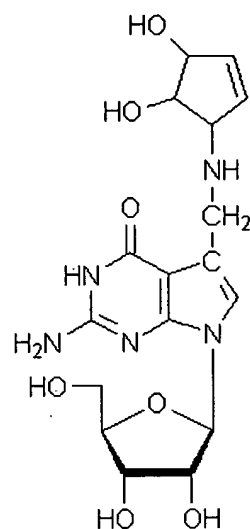


FIGURE 1

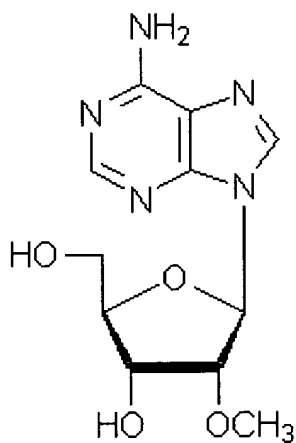
Pseudouridine(Ψ)



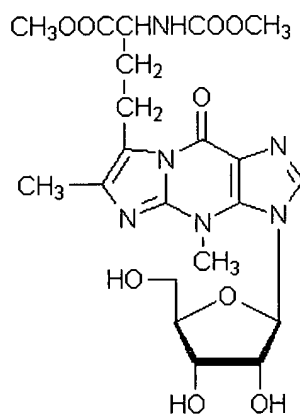
N6,N6-dimethyladenosine



Queuosine(Q)



2'-O-methyladenosine



Wybutosine(yW)

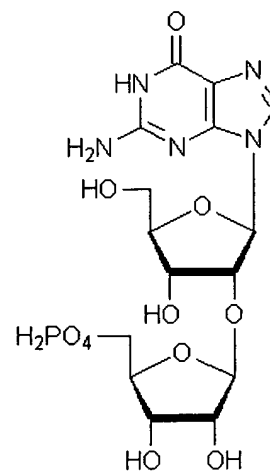
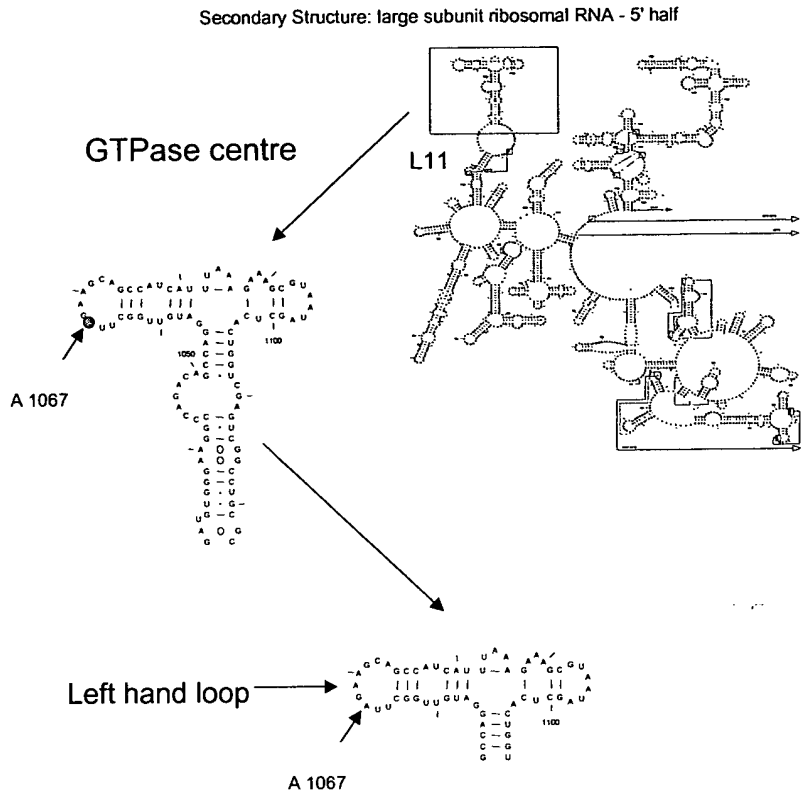
2'-O-ribosylguanosine
(phosphate)

FIGURE 2



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FIGURE 3

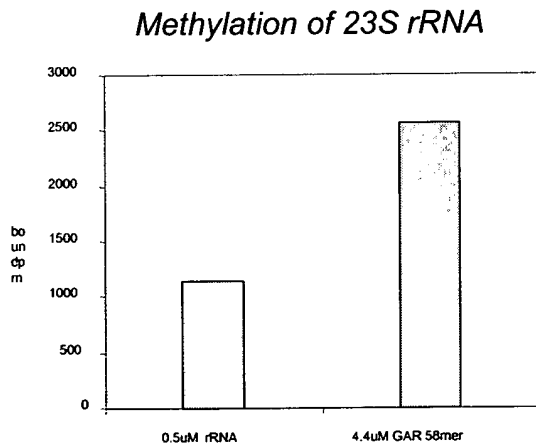
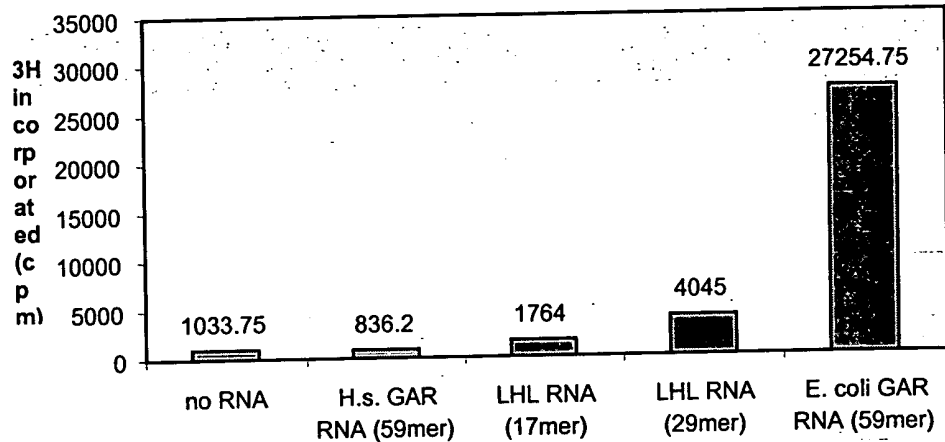
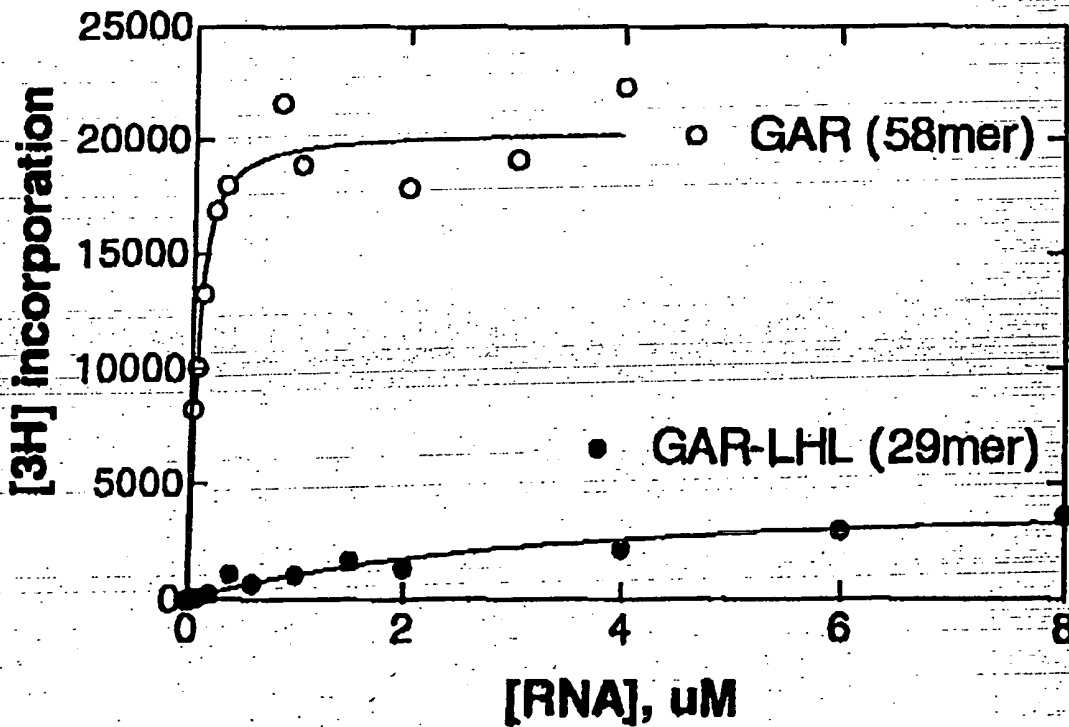


FIGURE 4A

Accessibility of the components of the GAR

**FIGURE 4B**

TSR methylates isolated GAR-LHL



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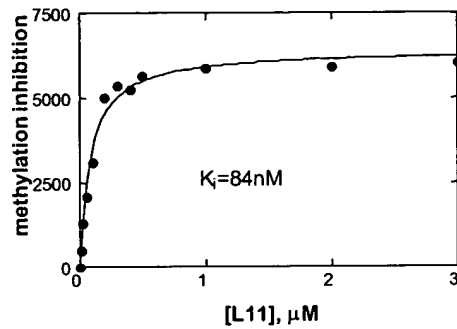
FIGURE 5*Binding of L11 by inhibition of methylation*

Figure 5

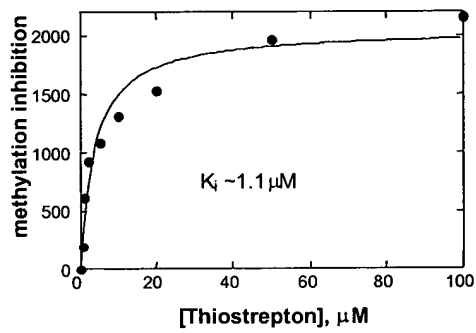
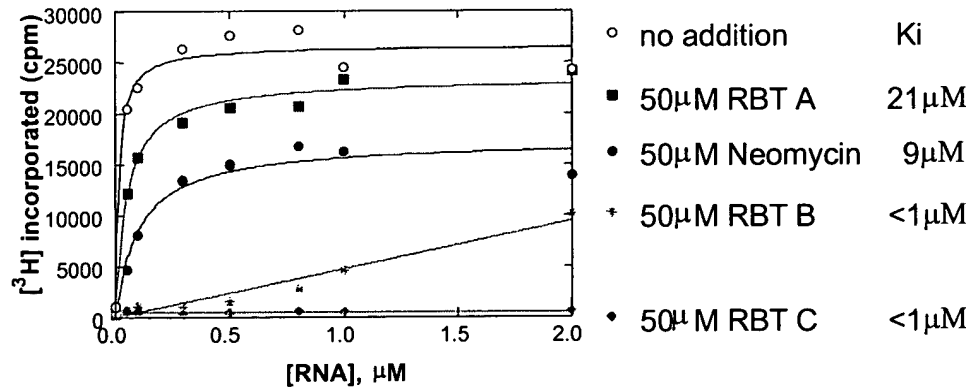
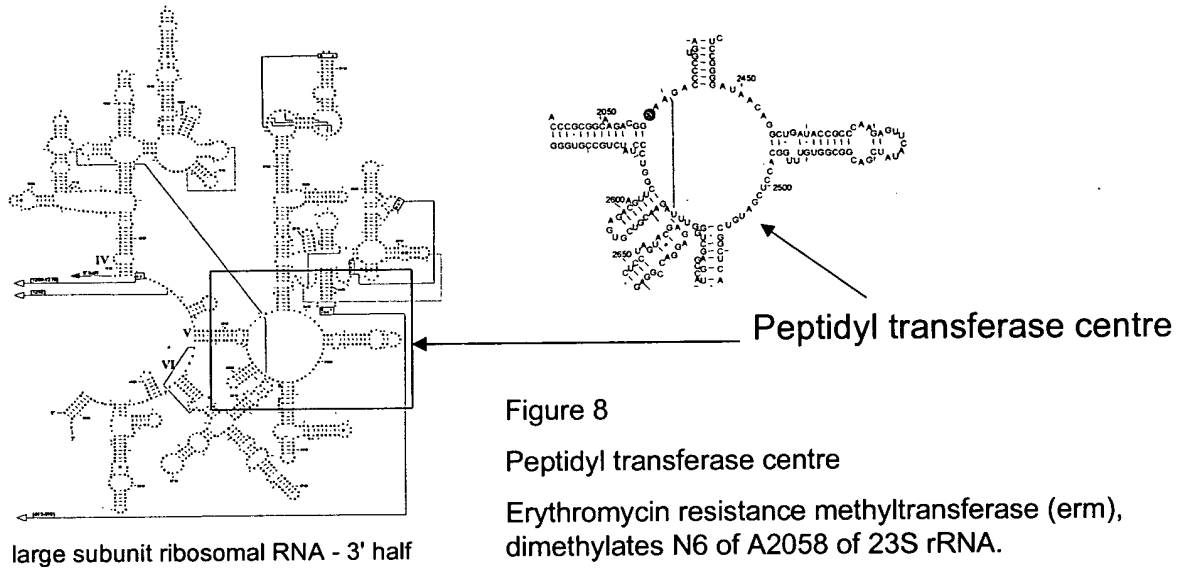
FIGURE 6*Binding of thiostrepton by inhibition of methylation***FIGURE 7***Inhibition of TSR methylation by RBT compounds*

FIGURE 8

Erythromycin resistance methyltransferase (erm)



T-30710-070300

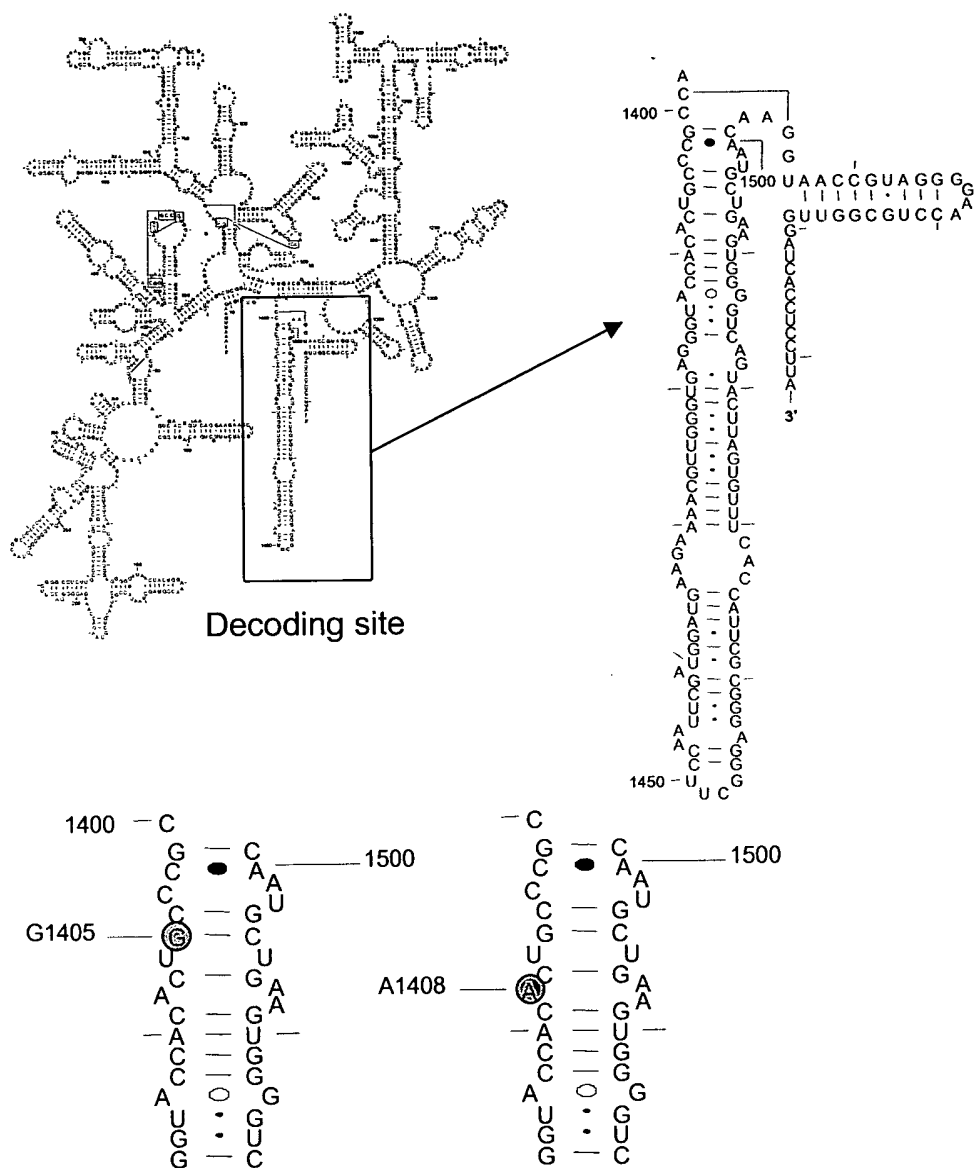
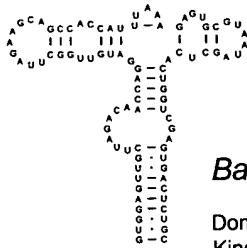
FIGURE 9**16S rRNA (*E. Coli*)**

Figure 9

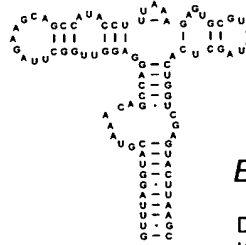
Methylation modifications in the decoding site of 16S rRNA that confer resistance to aminoglycoside antibiotics:

Methyltransferase converts G1405 to 7-methylguanosine

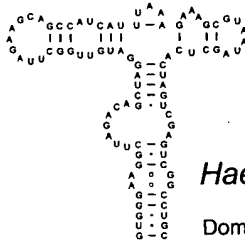
Methyltransferase converts A1408 to 1-methyladenosine

FIGURE 10**Secondary Structure: large subunit ribosomal RNA - 5' half***Bacillus subtilis*

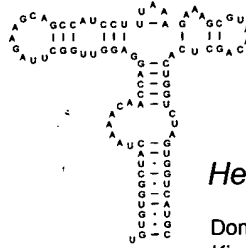
Domain: *Bacteria*
 Kingdom: *Gram-positive*
 Order: *Low G+C*

*Borrelia burgdorferi*

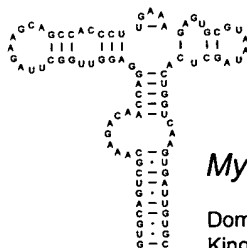
Domain: *Bacteria*
 Kingdom: *Spirochaetes*

*Haemophilus influenzae*

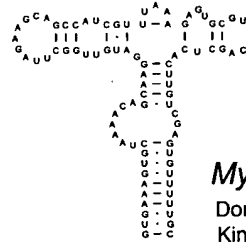
Domain: *Bacteria*
 Kingdom: *Purple Bacteria*
 Order: *gamma*

*Helicobacter pylori*

Domain: *Bacteria*
 Kingdom: *Purple Bacteria*
 Order: *epsilon ?*

*Mycobacterium leprae*

Domain: *Bacteria*
 Kingdom: *Gram-positive*
 Order: *High G+C*

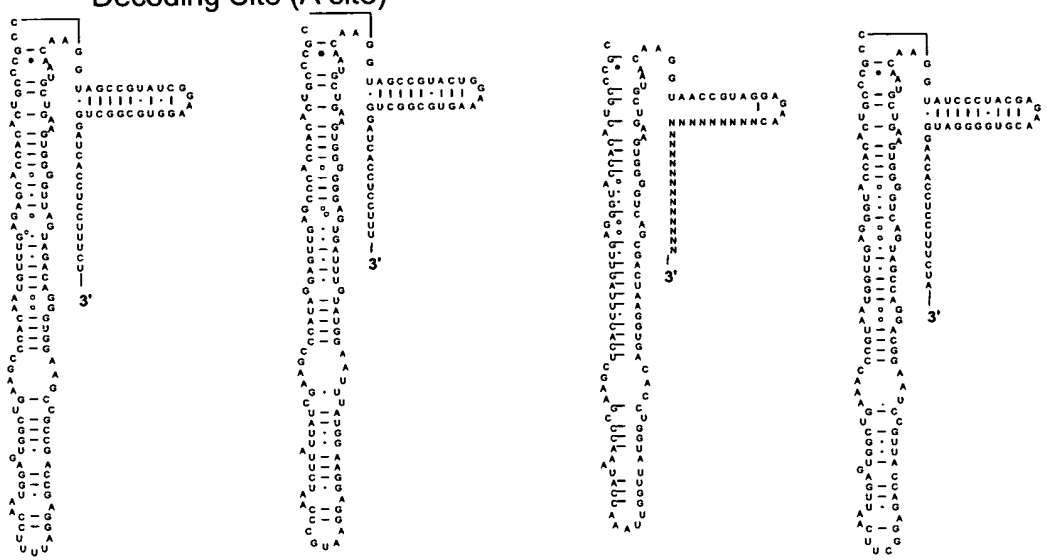
*Mycoplasma genitalium*

Domain: *Bacteria*
 Kingdom: *Gram-positive*
 Order: *Mycoplasmatales*

Fig10
 Sites accessible to the thiostrepton resistance methyltransferase
 In a range of bacteria

FIGURE 11

Secondary Structure: small subunit ribosomal RNA:
Decoding Site (A site)

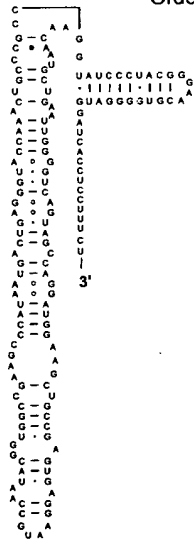


Bacillus subtilis
Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Low G+C*

Borrelia burgdorferi
Domain: *Bacteria*
Kingdom: *Spirochaetales*
Order: *Spirochaetales*

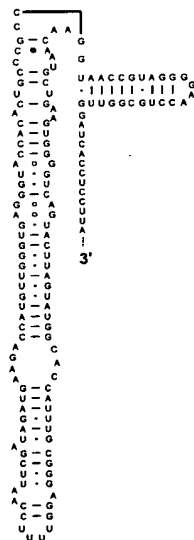
Campylobacter sputorum
Domain: *Bacteria*
Kingdom: *Purple Bacteria*
Order: *delta/epsilon*

Mycoplasma hypopneumoniae
Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmatales*



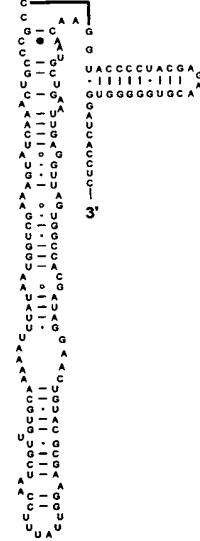
Clostridium innocuum

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmatales*



Haemophilus influenzae

Domain: *Bacteria*
Kingdom: *Purple Bacteria*
Order: *gamma*



Mycoplasma genitalium

Domain: *Bacteria*
Kingdom: *Gram-positive*
Order: *Mycoplasmatales*

Fig 11
The decoding site of 16SrRNA for range of bacteria

The "GTP" binding site

FIGURE 12

Secondary Structure: small subunit ribosomal RNA

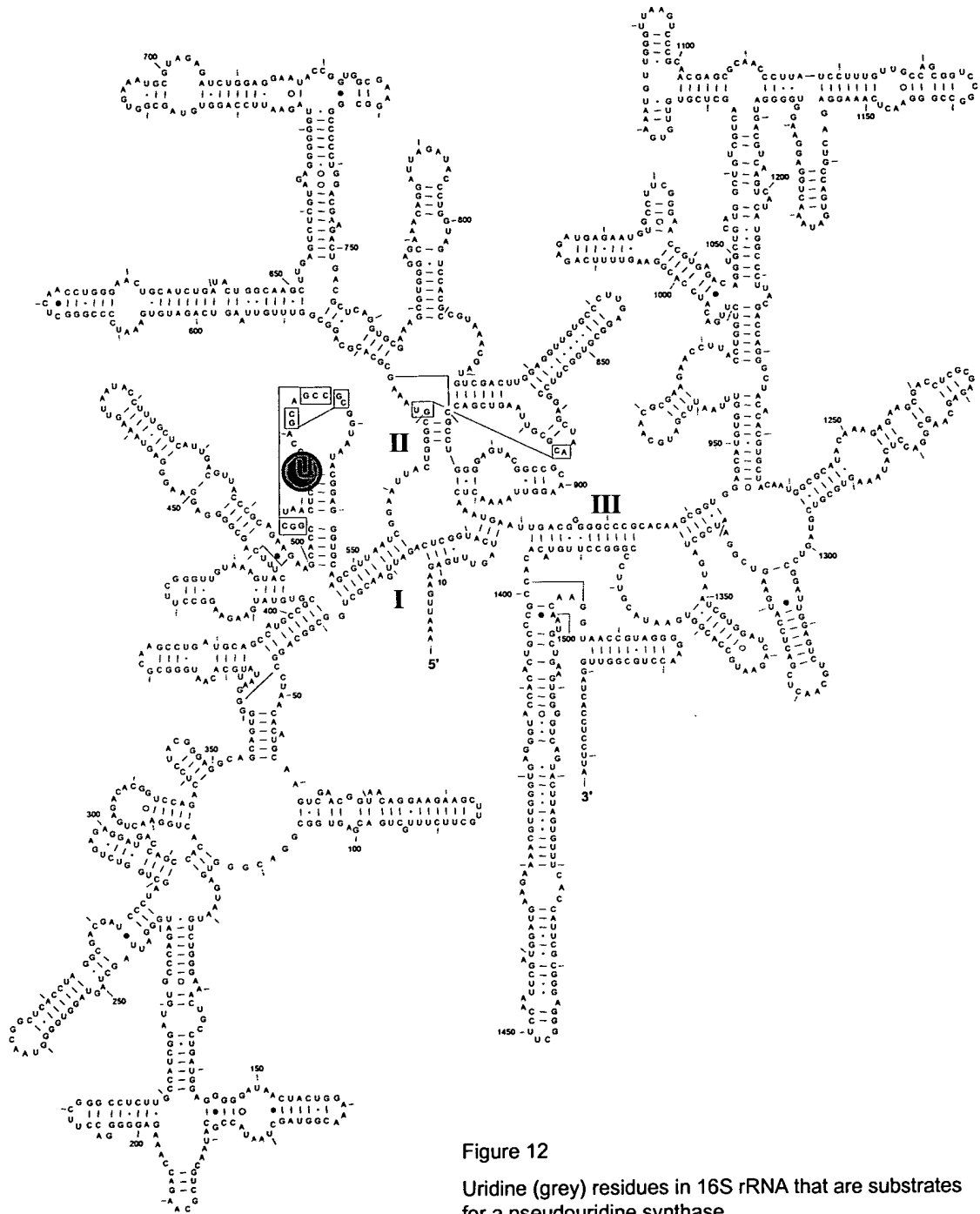


Figure 12
Uridine (grey) residues in 16S rRNA that are substrates for a pseudouridine synthase.

E. SCHERICHIA COLI
DOMAIN: Bacteria
KINGDOM: Purple Bacteria
ORDER: gamma
July 3, 1995 14:0
(10:59)

FIGURE 12

FIGURE 13

Secondary Structure: large subunit ribosomal RNA - 5' half

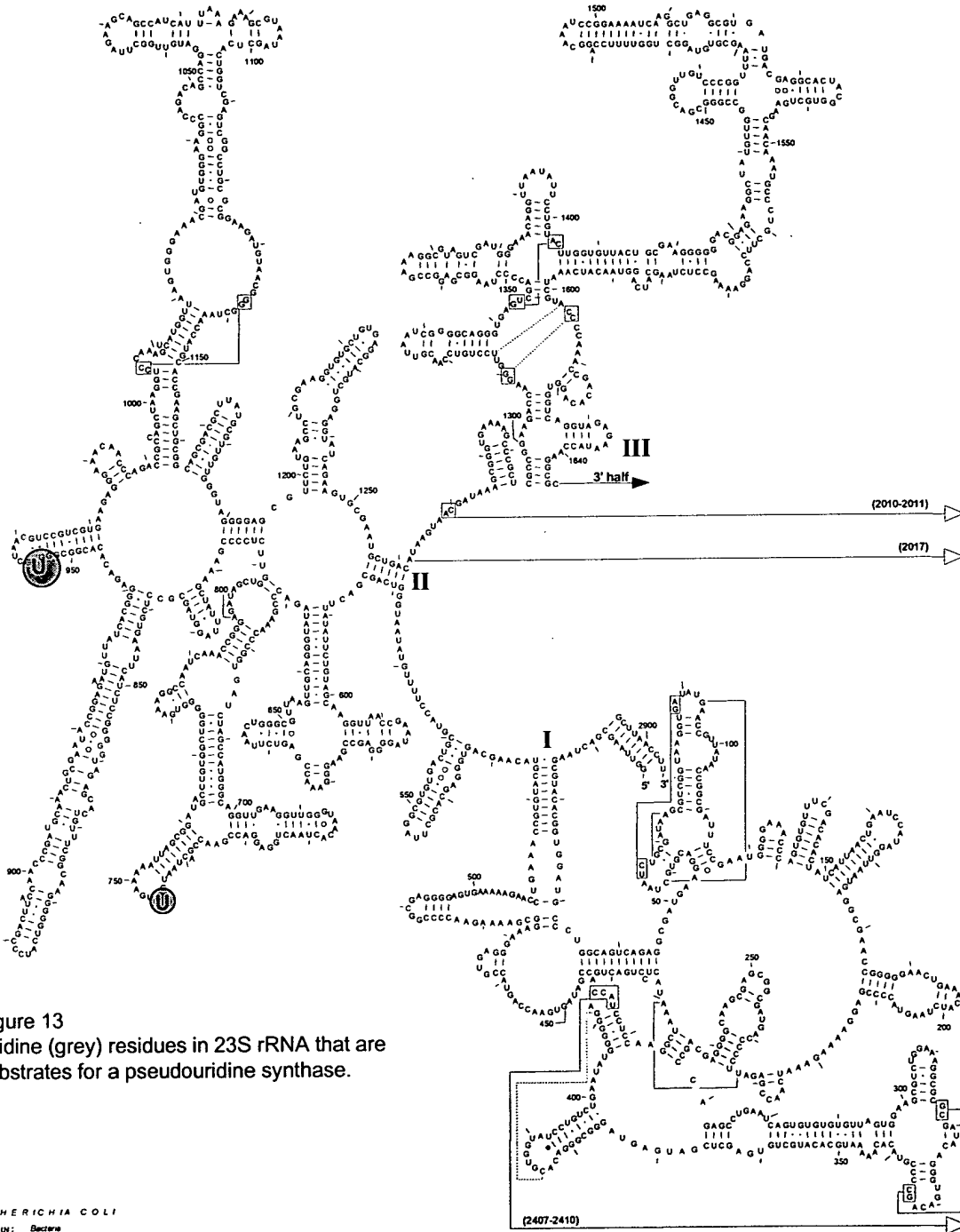


Figure 13
 Uridine (grey) residues in 23S rRNA that are
 substrates for a pseudouridine synthase.

ESCHERICHIA COLI
 DOMAIN: Bacteria
 KINGDOM: Purple Bacteria
 ORDER: gamma
 RELEASE: 2.3 (December 1994)
 (20102)

FIGURE 14

Secondary Structure: large subunit ribosomal RNA - 3' half

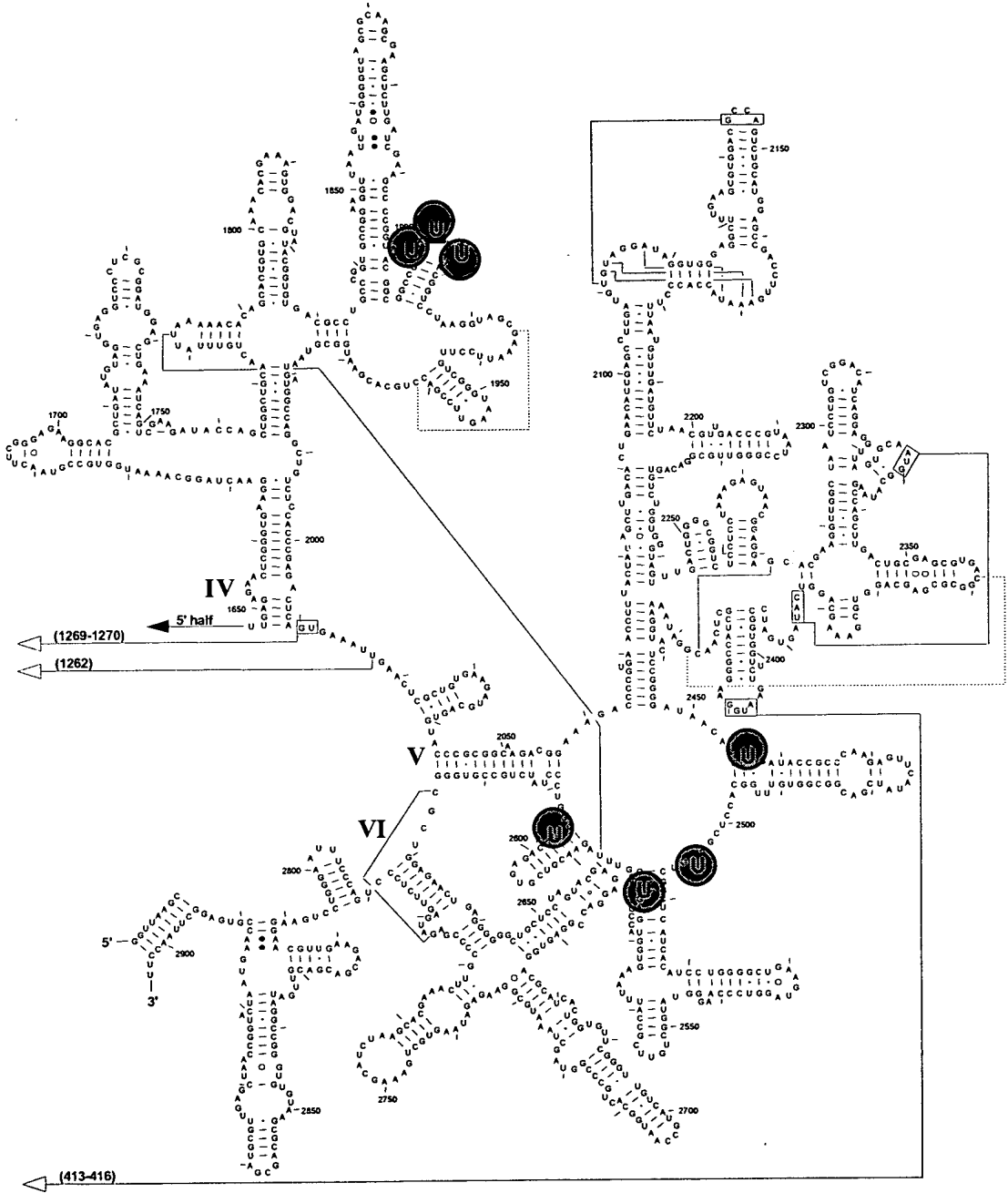
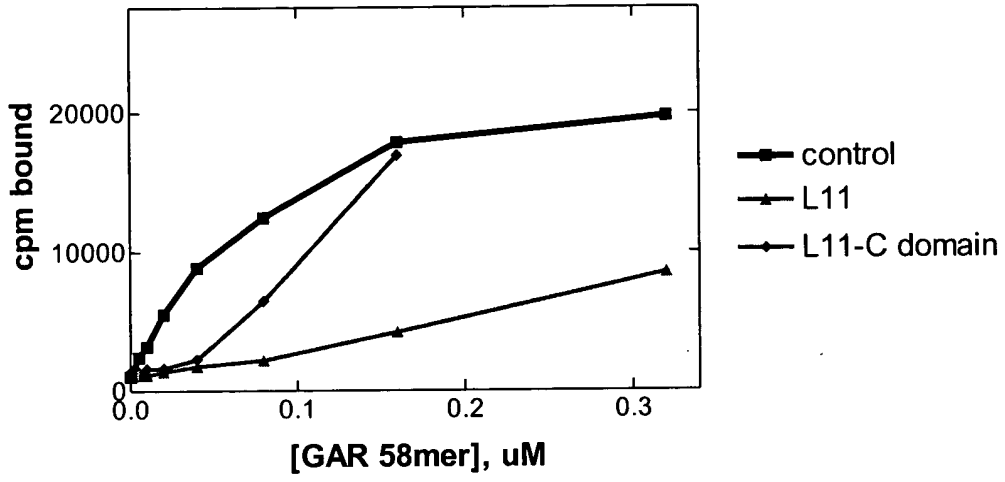


Figure 14

Uridine (grey) residues in 23S rRNA that are substrates for a pseudouridine synthase.

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FIGURE 15



12/17

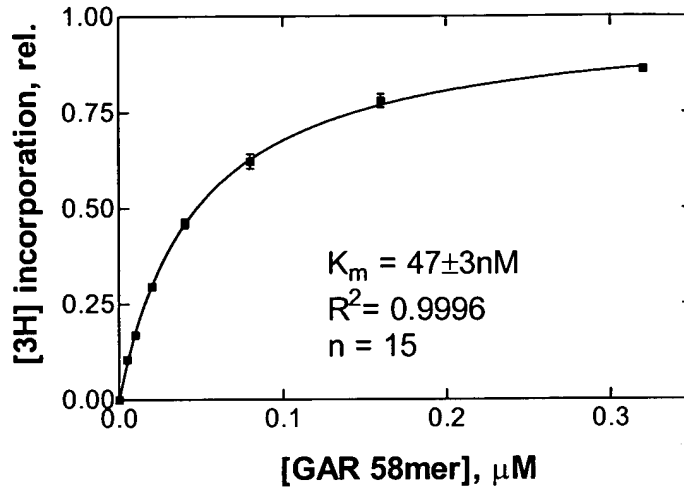
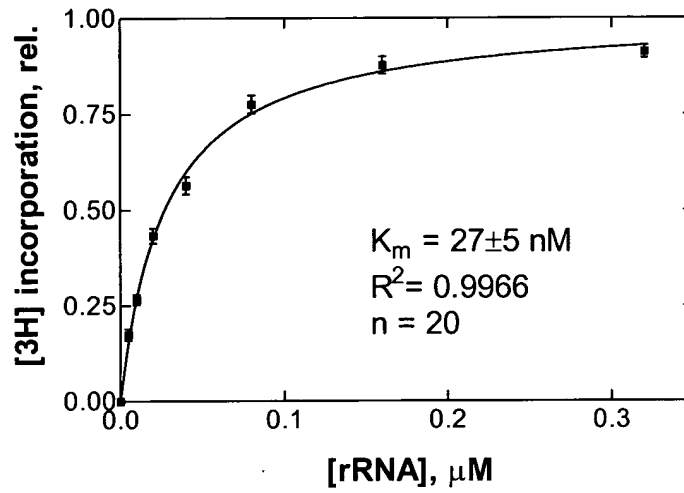
FIGURE 16**A****B**

FIGURE 17

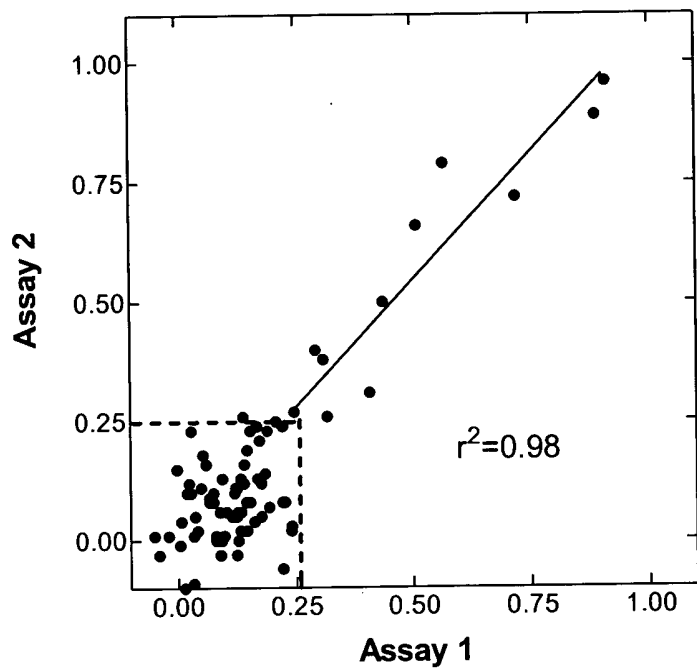
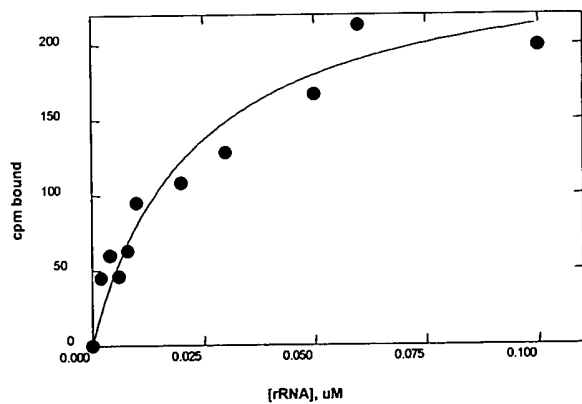


FIGURE 18



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FIGURE 19

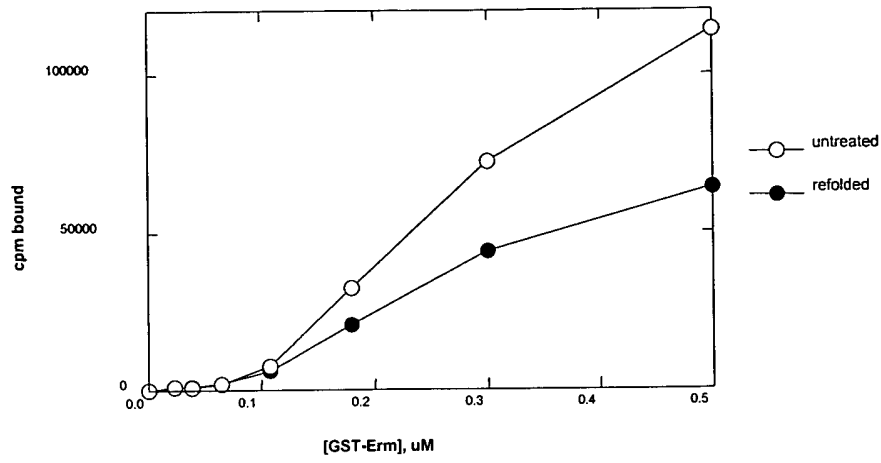
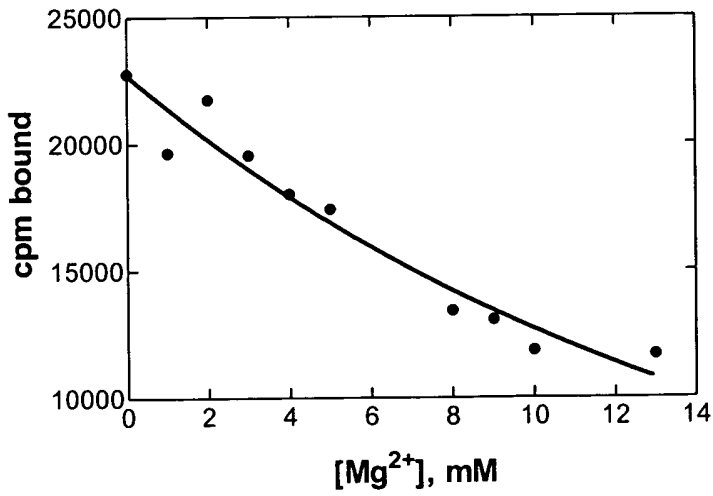
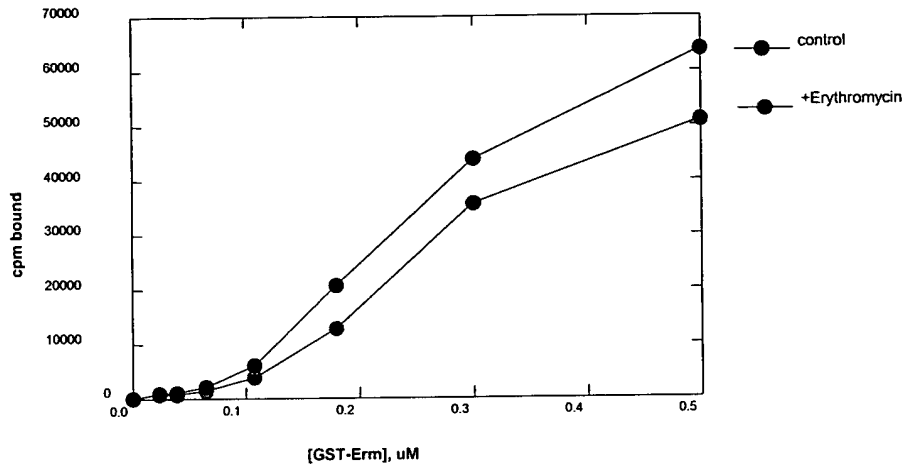


FIGURE 20



T. O. G. F. H. O. G. H. S. E. S. S. O.

FIGURE 21



11-01-01 11:00:00

FIGURE 22

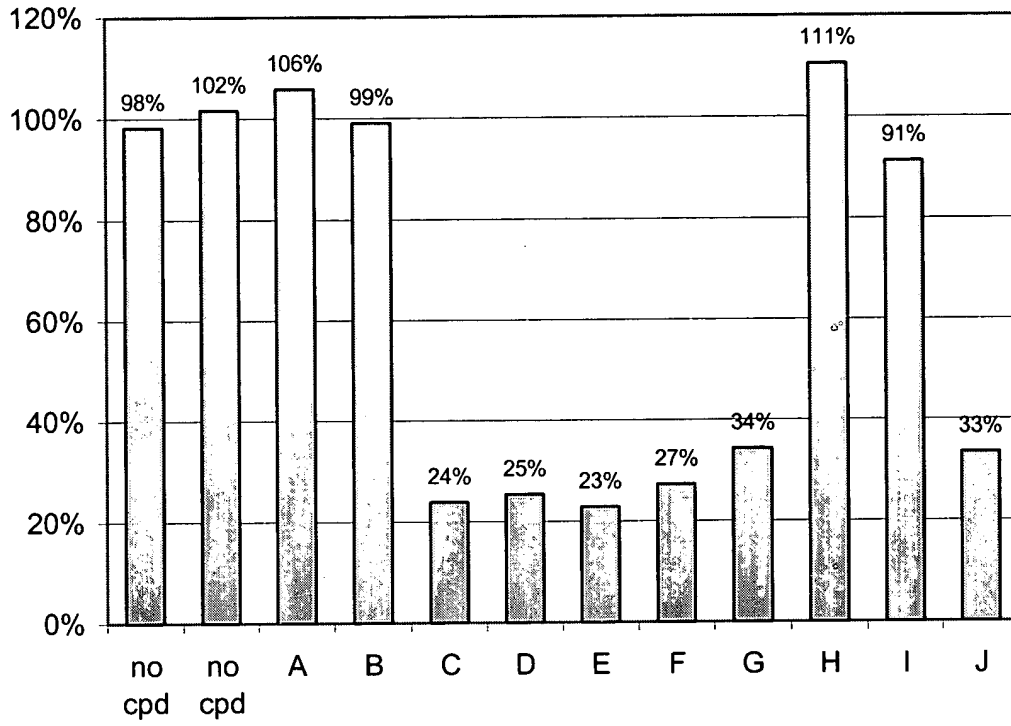


FIGURE 22